FIG. 1A

FIG. 1B

```
421 GGCGAGTGCTTGCCCCTGCCAGTGCTCCCTAACTGGATTGGAGGAGGCTATGGAACAAAG    480
102 G  E  C  L  P  L  P  V  L  P  N  W  I  G  G  G  Y  G  T  K     121

481 TACTGGAGCAGGAGGAGCTCCCAGGAGTGGCGGTGTGTCAATGACAAAACCCGTACCCAG    540
122 Y  W  S  R  R  S  S  Q  E  W  R  C  V  N  D  K  T  R  T  Q     141

541 AGAATCCAGCTGCAGTGCCAAGATGGCAGCACACGCACCTACAAAATCACAGTAGTCACT    600
142 R  I  Q  L  Q  C  Q  D  G  S  T  R  T  Y  K  I  T  V  V  T     161

601 GCCTGCAAGTGCAAGAGGTACACCCGGCAGCACAACGAGTCCAGTCACAACTTTGAGAGC    660
162 A  C  K  C  K  R  Y  T  R  Q  H  N  E  S  S  H  N  F  E  S     181

661 ATGTCACCTGCCAAGCCAGTCCAGCATCACAGAGAGCGGAAAAGAGCCAGCAAATCCAGC    720
182 M  S  P  A  K  P  V  Q  H  H  R  E  R  K  R  A  S  K  S  S     201

721 AAGCACAGCATGAGTTAGAACTCAGACTCCCATAACTAGACTTACTAGTAACCATCTGCT    780
202 K  H  S  M  S  *                                          206

781 TTACAGATTTGATTGCTTGGAAGACTCAAGCCTGCCACTGCTGTTTTCTCACTTGAAAGT    840
841 ATATGCTTTCTGCTTTGATCAAACCCAGCAAGCTGTCTTAAGTATCAGGACCTTCTTTGG    900
```

FIG. 2A

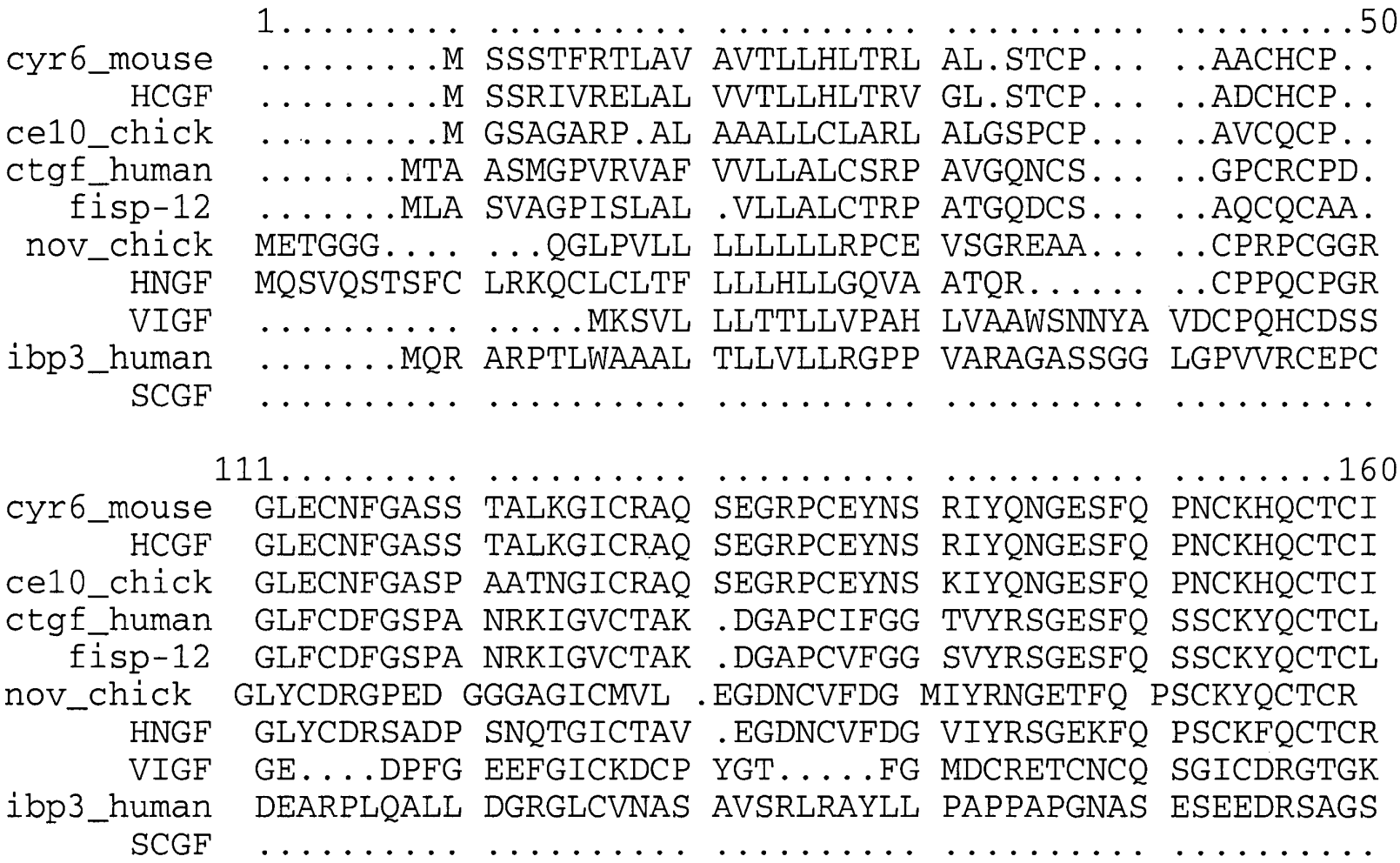

FIG. 2B

```
51..... ..... ..... ..... ..... .....110
..LEAPKCAP GVGLVR.... .DGCGCCKVC AKQLNED... .....C SKTQPCDHTK
..LEAPKCAP GVGLVR.... .DGCGCCKVC AKQLNED... .....C RKTQPCDHTK
..AAAPQCAP GVGLVP.... .DGCGCCKVC AKQLNED... .....C SRTQPCDHTK
..EPAPRCPA GVSLVL.... .DGCGCCRVC AKQLGEL... .....C TERDPCDPHK
..EAAPHCPA GVSLVL.... .DGCGCCRVC AKQLGEL... .....C TERDPCDPHK
CPAEPPRCAP GVPAVL.... .DGCGCCLVC ARQRGES... .....C SPLLPCDESG
CPATPPTCAP GVRAVL.... .DGCSCCLVC ARQRGES... .....C SDLEPCDESS
ECKSSPRCKR TVL..... .DDCGCCRVC AAGRGETCYR TVSGMDGMKC GPGLRCQPSN
DARALAQCAP PPAVCAELVR EPGCGCCLTC ALSEGQPC.. ...GIYTERC GSGLRCQPSP
..... ..... ..... ..... ..... .....

161..... ..... ..... ..... ..... .....220
D.GAVGCIPL CPQELSLPNL GCPNPRLVKV SGQCCEEWVC DEDSIKDSLD DQDDL....L
GWRRGACIPL CPQELSLPNL GCPNPRLVKV TGQCCEEWVC DEDSIKDPME DQDGLLGKGL
D.GAVGCIPL CPQELSLPNL GCPSPRLVKV PGQCCEEWVC DES..KDALE ELEGFFSKEF
D.GAVGCMPL CSMDVRLPSP DCPFPRRVKL PGKCCEEWVC DEP..... ..KDQTVVGP
D.GAVGCVPL CSMDVRLPSP DCPFPRRVKL PGKCCKEWVC DEP..... ..KDRTAVGP
D.GQIGCLPR CNLGLLLPGP DCPFPRKIEV PGECCEKWVC DPR..... ..DEVLLGGF
D.GQIGCVPR CQLDVLLPEP NCPAPRKVEV PGECCEKWIC GPD..... ..EEDSLGGL
CL..... ..... ..KFPFFQYS VTKSSNRFVS LTEHDMASGD GNIVREEVVK
VESPSVSSTH RVSDPKFHPL HSKIIIIKKG HAKDSQRYK. .VDYESQSTD TQNFSSESKR
..... ..... ..... ..... ..... .....
```

FIG 2.C

```
          221..... ..... ..... ..... .....270
cyr6_mouse  GLDASEVELT RNNELIAIGK GSSLKRLPVF GTEP..RVLF NPLHAHGQKC
      HCGF  GFDASEVELT RNNELIAVGK GSSLKRLPVF GMEP..RILY NPL..QGQKC
ce10_chick  GLDASEGELT RNNELIAIVK G.GLKMLPVF GSEPQSRAFE NP.....KC
ctgf_human  ALAAYRLEDT ..... .....F GPDPTMI... .....RANC
   fisp-12  ALAAYRLEDT ..... .....F GPDPTMM... .....RANC
 nov_chick  AMAAYRQEAT ..... .....L GIDVSDS... .....SANC
      HNGF  TLAAYRPEAT ..... .....L GVEVSDS... .....SVNC
      VIGF  ENAAGSPVMR KWLNPR.... ..... ..... .....
ibp3_human  ETEYGPCRRE MEDTLNHLKF LNVLSPRGVH IPNCDKKGFY KKKQCRPSKG
      SCGF  ...MLPPAIH FYLLPLACIL MKSCLAFKND ATEILYSHVV KPVPAHPSSN


          331..... ..... ..... ..... .....380
cyr6_mouse  TKKSPEPVRF TYAGCSSVKK YRPKYCGSCV DGRCCTPLQT RTVKMRFRCE
      HCGF  TKKSPEPVRF TYAGCLSVKK YRPKYCGSCV DGRCCTPQLT RTVKMRFPCE
ce10_chick  TKKSPSPVRF TYAGCSSVKK YRPKYCGSCV DGRCCTPQQT RTVKIRFRCD
ctgf_human  TPKISKPIKF ELSGCTSMKT YRAKFCGVCT DGRCCTPHRT TTLPVEFKCP
   fisp-12  TPKIAKPVKF ELSGCTSVKT YRAKFCGVCT DGRCCTPHRT TTLPVEFKCP
 nov_chick  TKKSMKAVRF EYKNCTSVQT YKPRYCGLCN DGRCCTPHNT KTIQVEFRCP
      HNGF  TKKSLKAIHL QFKNCTSLHT YKPRFCGVCS DGRCCTPHNT KTIQAEFQCS
      VIGF  ..... ..... ..... ..... .....
ibp3_human  ..... ..... ..... ..... .....
      SCGF  ....PLPVLP NWIGGGYGTK YWSR...RSS QEWRCVNDKT RTQRIQLQCQ
```

FIG 2D

```
271..... ..........  ..........  ..........  ..........  .....330
IVQTTSWSQC SKSCGTGIST RVTNDNPECR LVKETRICEV RPCGQPVY.S SLKKGKKCSK
IVQTTSWSQC SKTCGTGIST RVTNDNPECR LVKETRICEV RPCGQPVY.S SLKKGKKCSK
IVQTTSWSQC SKTCGTGIST RVTNDNPDCK LIKETRICEV RPCGQPSY.A SLKKGKKCTK
LVQTTEWSAC SKTCGMGIST RVTNDNASCR LEKQSRLCMV RPCEADLEE. NIKKGKKCIR
LVQTTEWSAC SKTCGMGIST RVTNDNTFCR LEKQSRLCMV RPCEADLEE. NIKKGKKCIR
IEQTTEWSAC SKSCGMGFST RVTNRNQQCE MVKQTRLCMM RPCEN..EEP SDKKGKKCIQ
IEQTTEWTAC SKSCGMGFST RVTNRNRQCE MLKQTRLCMV RPCEQEPEQP TDKKGKKCLR
.......... ..........  ..........  ..........  ..........  ..........
RKRGFCWCVD KYGQPLPGYT TKGKEDVHCY SMQSK.....  ..........  ..........
STLNQARNGG RHFSNTGL.D RNTRVQVGCR ELRSTKYISD GQCTSISPLK ELVCAGECL.


381..... ..........  ..........  ..........  ..........  .....440
DGEMFSKNVM MIQSCKCNYN CPHPNEASFR LYSLFNDIHK FRD.......  ..........
DGETFSKNVM MIQSSKCNYN CPHANEAAFP FYRLF.....  ..........  ..........
DGETFTKSVM MIQSCRCNYN CPHANEA.YP FYRLVNDIHK FRD.......  ..........
DGEVMKKNMM FIKTCACHYN CPGDND.IFE SLYYRKMYGD MA........  ..........
DGEIMKKNMM FIKTCACHYN CPGDND.IFE SLYYRKMYGD MA........  ..........
QGKFLKKPMM LINTCVCHGN CPQSNNAFFQ PLDPMSSEAK I.........  ..........
PGQIVKKPVM VIGTCTCHTN CPKNNEAFLQ ELELKTTRGK M.........  ..........
.......... ..........  ..........  ..........  ..........  ..........
.......... ..........  ..........  ..........  ..........  ..........
DGSTRTYKIT VVTACKCKRY TRQHNESSHN FESMSPAKPV QHHRERKRAS KSSKHSMS
```